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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/503,089

DATE: 03/03/2000

TIME: 11:28:35

Input Set: I503089.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

E--> 1 <110> PATEL, AMANDA J.
2 HONORE, ERIC
3 LESAGE, FLORIAN
4 ROMÉY, GEORGES
5 LAZDUSKI, MICHEL
6 <120> A method for the identification of anesthetics
7 <130> f17b12prov3-humanTREK
8 <140> US/09/503,089
9 <141> 2000-02-11
10 <160> 4 (see last page)
11 <170> Wordperfect 8.0

ERRORED SEQUENCES FOLLOW

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14 <212> ADN DNA
15 <213> Homo sapiens
16 <220>
17 <221> CDS
18 <222> (1) .. (1236)
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22 1 5 10 15
23 aaa ccg agg ctc tcg ttt tcc acg aaa ccc aca gtg ctt gct tcc cgg 96
24 Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg
25 20 25 30
26 gtg gag agt gac acg acc att aat gtt atg aaa tgg aag acg gtc tcc 144
27 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
28 35 40 45
29 acg ata ttc ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg 192
30 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
31 50 55 60
32 ttc aaa gca ttg gag cag cct cat gag att tca cag agg acc acc att 240
33 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
34 65 70 75 80
35 gtg atc cag aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg 288
36 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
37 85 90 95
38 acg gag ctg gat gaa ctc att cag caa ata gtg gca gca ata aat gca 336
39 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala

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44	ttg	gga	agt	tcc	ttc	ttc	ttt	gct	ggc	act	ggt	att	aca	acc	ata	gga	432
45	Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	
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49			145					150					155			160	
50	atc	tat	gcc	tta	ctg	gga	att	ccc	ctc	ttt	ggg	ttt	ctc	ttg	gct	gga	528
51	Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	
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54	Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	
55			180						185				190				
56	gaa	gat	acg	ttt	att	aag	tgg	aat	gtt	agt	cag	acc	aag	att	cgc	atc	624
57	Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile	
58			195					200					205				
59	atc	tca	aca	atc	ata	ttt	ata	cta	ttt	ggc	tgt	gta	ctc	ttt	gtg	gct	672
60	Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala	
61			210					215					220				
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63	Leu	Pro	Ala	Ile	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp	
64			225					230					235			240	
65	gcc	att	tat	ttt	gtg	gtt	atc	act	cta	aca	act	att	gga	ttt	ggg	gac	768
66	Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	
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68	tac	gtt	gca	ggg	gga	tcc	gat	att	gaa	tat	ctg	gac	ttc	tat	aag	cct	816
69	Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro	
70			260						265				270				
71	gtc	gtg	tgg	ttc	tgg	atc	ctt	gta	ggg	ctt	gct	tac	ttt	gct	gct	gtc	864
72	Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val	
73			275					280					285				
74	ctg	agc	atg	att	gga	gat	tgg	ctc	cga	gtg	ata	tct	aaa	aag	aca	aaa	912
75	Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys	
76			290					295					300				
77	gaa	gag	gtg	gga	gag	ttc	aga	gca	cac	gct	gct	gag	tgg	aca	gcc	aac	960
78	Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asn	
79			305					310					315			320	
80	gtc	aca	gcc	gaa	ttc	aaa	gaa	acc	agg	agg	cga	ctg	agt	gtg	gag	att	1008
81	Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile	
82				325						330				335			
83	tat	gac	aag	ttc	cag	cgg	gcc	acc	tcc	atc	aag	cgg	aag	ctc	tcg	gca	1056
84	Tyr	Asp	Lys	Phe	Gln	Arg	Ala	Thr	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Ala	
85			340						345					350			
86	gaa	ctg	gct	gga	aac	cac	aat	cag	gag	ctg	act	cct	tgt	agg	agg	acc	1104
87	Glu	Leu	Ala	Gly	Asn	His	Asn	Gln	Glu	Leu	Thr	Pro	Cys	Arg	Arg	Thr	
88			355						360					365			
89	ctg	tca	gtg	aac	cac	ctg	acc	aac	gag	agg	gat	gtc	ttg	cct	ccc	tta	1152

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92	ctg aag act gag agt atc tat ctg aat ggt ttg acg cca cac tgt gct	1200
93	Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala	
94	385 390 395 400	
95	ggt gaa gag att gct gtg att gag aac atc aaa tag	1236
96	Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys	
97	405 410	

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108	gaagaggggc tgcagtgatc accccctcgc tgagccccgg ggagagagccc agccgcccggc	180
109	cgagcgcacg gagccacggg ccgagcgcac ccagggcccc cgccgggaccc caggcggcca	240
110	cgcaatcggg gtgacccatc gcgcgggggg gcgtcgtcgt ccgatcccaa cttggcctcg	300
111	gcctcgcctt ctgcccagcc tgccaccgct ggtgtcctct ccttcgggag atttcgtttc	360
112	ttctcacgct cccccctcta taccctccc gcctccagcc ccgctctccc caccttgtaa	420
113	aacaaagccg gggaaaatgc ctaccctgtc agctcggagc gcgcagcccc tcttgaata	480
114	agg atg gcg gcc cct gac ttg ctg gat ccc aag tct gct gct cag aac	528
115	Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn	
116	1 5 10 15	
117	tcc aaa ccg agg ctc tca ttc tcc tca aaa ccc acc gtg ctt gct tcc	576
118	Ser Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser	
119	20 25 30	
120	cgg gtg gag agt gac tcg gcc att aat gtt atg aaa tgg aag aca gtc	624
121	Arg Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val	
122	35 40 45	
123	tcc acg att ttc ctg gtg gtc gtc ctc tac ctg atc atc gga gcc gcg	672
124	Ser Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala	
125	50 55 60	
126	gtg ttc aag gca ttg gag cag cct cag gag att tcc cag agg acc acc	720
127	Val Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr	
128	65 70 75	
129	att gtg atc cag aag cag acc ttc ata gcc cag cat gcc tgc gtc aac	768
130	Ile Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn	
131	80 85 90 95	
132	tcc acc gag ctg gac gaa ctc atc cag caa ata gtg gca gca ata aac	816
133	Ser Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn	
134	100 105 110	
135	gca ggg att atc ccc tta gga aac agc tcc aat caa gtt agt cac tgg	864
136	Ala Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp	
137	115 120 125	
138	gac ctc gga agc tct ttc ttc ttt gct ggt act gtt atc aca acc ata	912

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139	Asp	Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	
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142	Gly	Phe	Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	
143			145					150					155				
144	atc	atc	tat	gcc	ttg	ctg	gga	att	ccc	ctc	ttt	ggc	ttt	cta	ctg	gct	1008
145	Ile	Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	
146			160					165					170			175	
147	ggg	gtt	ggt	gat	cag	cta	gga	act	ata	ttt	gga	aaa	gga	att	gcc	aaa	1056
148	Gly	Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	
149					180					185					190		
150	gtg	gaa	gac	aca	ttt	att	aag	tgg	aat	gtt	agt	cag	acg	aag	att	cgt	1104
151	Val	Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	
152				195					200					205			
153	atc	atc	tcc	acc	atc	atc	ttc	atc	ctg	ttt	ggc	tgt	gtc	ctc	ttt	gtg	1152
154	Ile	Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	
155			210					215					220				
156	gct	ctc	cct	gcg	gtc	ata	ttc	aag	cac	ata	gaa	ggc	tgg	agc	gcc	ctg	1200
157	Ala	Leu	Pro	Ala	Val	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	
158			225					230					235				
159	gac	gct	atc	tat	ttt	gtg	gtt	atc	act	ctg	acg	acc	att	gga	ttt	gga	1248
160	Asp	Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	
161			240					245					250			255	
162	gac	tac	gtg	gca	ggt	gga	tca	gac	att	gaa	tat	ctg	gac	ttc	tac	aag	1296
163	Asp	Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	
164				260						265				270			
165	cct	gtg	gtg	tgg	ttc	tgg	atc	ctc	gtt	ggg	ctg	gcc	tac	ttt	gca	gct	1344
166	Pro	Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	
167				275					280					285			
168	gtt	ctg	agc	atg	att	ggg	gac	tgg	cta	cgg	gtg	atc	tct	aag	aag	acg	1392
169	Val	Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	
170			290					295					300				
171	aag	gaa	gag	gtg	gga	gag	ttc	aga	gcg	cat	gcc	gct	gag	tgg	aca	gcc	1440
172	Lys	Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	
173			305					310					315				
174	aat	gtc	acg	gcc	gag	ttc	aag	gaa	acg	agg	agg	cgg	ctg	agc	gtg	gag	1488
175	Asn	Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	
176			320					325					330			335	
177	atc	tac	gac	aag	ttc	cag	cgt	gcc	aca	tcc	gtg	aag	cgg	aag	ctc	tcc	1536
178	Ile	Tyr	Asp	Lys	Phe	Gln	Arg	Ala	Thr	Ser	Val	Lys	Arg	Lys	Leu	Ser	
179				340						345				350			
180	gca	gag	ctg	gcg	ggc	aac	cac	aac	cag	gaa	ctg	act	ccg	tgt	agg	agg	1584
181	Ala	Glu	Leu	Ala	Gly	Asn	His	Asn	Gln	Glu	Leu	Thr	Pro	Cys	Arg	Arg	
182			355						360					365			
183	acc	ctg	tct	gtg	aac	cac	ctg	acc	agc	gag	agg	gaa	gtc	ctg	cct	ccc	1632
184	Thr	Leu	Ser	Val	Asn	His	Leu	Thr	Ser	Glu	Arg	Glu	Val	Leu	Pro	Pro	
185			370						375					380			
186	ttg	ctg	aag	gct	gag	agc	atc	tat	ctg	aac	ggt	ctg	aca	cca	cac	tgt	1680
187	Leu	Leu	Lys	Ala	Glu	Ser	Ile	Tyr	Leu	Asn	Gly	Leu	Thr	Pro	His	Cys	
188			385					390						395			

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193	gtagcattta aacattgtgc atggtgacct caaagggaaa gcaaatagaa aacacccatc	1849
194	tggtcacctt acatccaggg aggggtgttg cccgaggcgg cactctgagg atgccgtgtg	1909
195	ctgtccgctg agtgctgagt gatggacagg cagtgtctga tgccttttgt gccagactg	1969
196	tttccctccc ccctctctcc taacgtgcca taaggcctat gaatgaatct gaatgctttg	2029
197	ctggtcatgt agattggagg gatcagccct tggtttttca tggttcacct aactgagcct	2089
198	ggatactgac cacttaggga tgacaacatt tctttttgta aatggcgaga aattcttacg	2149
199	cagcctttta cctaagaaat tttctgccag tgccttatct tatgaagaaa caagaccctg	2209
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204	tggtagagct atatatatgt acagagtaat aattcccagg ccggtaacct tggctgcttc	2509
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206	atttttaaaag gcagaagaag acatgagcac atacatctgt aatctacgtg atgtgataag	2629
207	aaaactgttc agactggtat tgcaagggtga tctcagacag tcgatatgga ttcattctga	2689
208	tgagaagaaa acagcgagac cacgtgtcgt gcgcagtagc tcatacaggg ctcactgtca	2749
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212	tttgacatg gagagataca gactgctggc ataggtcgtc tctaacagta gagaaaacgc	2989
213	cgattagcac aatctaaatc ccccagtag ctttttgttt aggataagag aaggctggta	3049
214	attcacttaa tttaaattta tatectataa ttcttttttg atgtttcaag attcagaaaa	3109
215	agtccagtcc ctgcatctag caaacggcgg ccttttctc tgtgccgta cttacatcta	3169
216	ctgaacactg tatatgtaat ttttaaattt ttaaagcgca gaaggaaaat gattcttcta	3229
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220	agtactttta taaacctatg aagattctaa ccaaaatttt aaaatgtcgg gttcctttac	3469
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See next page

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<212> PRT

<213> Mus sp.

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 65 70 75 80
 Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95
 Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
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 Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
 115 120 125
 Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
 130 135 140
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 180 185 190
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 260 265 270
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 325 330 335
 Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly Arg
 340 345 350
 Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg
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 Arg Gly Leu Met Lys Arg Arg Ser Ser Val
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*last sequence in file**>22207 <- insert this numeric identifier, series**22237 is shown*

Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

PMI